IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Goddard et al.	Attorney's Docket No: 39780-2630P1C4
Serial No:	09/978,191	Group Art Unit: 1646
Filed:	October 15, 2001	Examiner: O'Hara, Eileen B.

For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

DECLARATION OF AUDREY GODDARD, Ph.D., PAUL J. GODOWSKI, Ph.D., AUSTIN GURNEY, Ph.D., MARGARET A. ROY and WILLIAM I. WOOD, Ph.D.UNDER 37 CFR 1.131

We, Audrey Goddard, Ph.D., Paul J. Godowski, Ph.D., Austin Gurney, Ph.D., Margaret Roy and William I. Wood, Ph.D. do hereby declare and say as follows:

1. We are the inventors of the above-identified application.

2. We have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by Holtzman *et al.*, U.S. Published Patent Application 20020028508, with effective priority date April 23, 1998 (09/065,363), and Sheppard *et al.*, U.S. Published Patent Application 20030166907, with effective priority date June 18, 1997 (09/050,143)

3. The polypeptide comprising the amino acid sequence of residues 35-273 of SEQ ID NO:506 and the nucleic acid sequence of nucleotides 603-1220 of SEQ ID NO:505 in the above-identified application in the United States were sequenced and cloned prior to June 18, 1997.

4. At the time the above polypeptide was cloned and sequenced, one of the inventors, Austin Gurney, was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA encoding the polypeptide comprising the amino acid sequence of residues 35-273 of SEQ ID NO:506.

5. At the time the above polypeptide was cloned and sequenced, one of the inventors, Audrey Goddard, was responsible for overseeing the sequencing of nucleotides encoding novel polypeptides, including the polypeptide having the amino acid sequence of residues 35-273 of SEQ ID NO: 506 in the above-identified application.

6. At the time the nucleotide encoding the above polypeptide was cloned and sequenced, one of the inventors, William I. Wood, was responsible for overseeing the homology searches for novel polypeptides, including that for the polypeptide having the amino acid sequence of residues 35-273 of SEQ ID NO: 506 in the above-identified application.

7. The PRO213 polypeptide shown in SEQ ID NO:2 is encoded by a cDNA sequence referred to as DNA30943-1163 and shown in Figure 2 of the above-identified application.

8. A cDNA sequence DNA30943-1163 is identified as SEQ ID NO:1 and shown in Figure 1 of the above-identified application.

9. The PRO213 nucleic acid sequence was found to contain sequence errors. Therefore, the PRO213 nucleic acid sequence was resequenced and designated as 213-1 nucleic acid sequence and the translated polypeptide was designated as the PRO213-1 polypeptide.

10. The PRO213-1 polypeptide shown in SEQ ID NO:506 is encoded by a cDNA sequence referred to as DNA30943-1-1163-1 and shown in Figure 213 of the above-identified application..

11. A cDNA sequence DNA30943-1-1163-1 is identified as SEQ ID NO:505 and shown in Figure 212 of the above-identified application.

12. Copies of the pages from the GSeqEdit database and GenenGenes database which report the cloning, sequencing and functional data for the PRO213 and PRO213-1 polypeptide sequences, including its homology to human gas6, as well as the cloning, and sequencing data for the nucleic acid sequence encoding the PRO213 and PRO213-1 polypeptides are attached to this declaration (with the dates redacted) as Exhibit A.

13. The GSeqEdit report shows the full-length nucleic acid sequence for DNA30943-1-1163-1 and the full-length PRO213-1 polypeptide encoded by DNA30943-1-1163-1. The full-length nucleic acid sequence for PRO213-1 (DNA30943-1-1163-1) shown in the report includes the sequence corrections made to PRO213 (DNA30943-1163) indicated below the sequence, for example, as seen on page 5 of the report. The full-length nucleic acid sequence for PRO213 (DNA30943-1163) is the sequence shown in the GSeqEdit report without the indicated corrections.

14. The amino acid sequence of residues 1-49 of PRO213 is shown in GSeqEdit report on pages 4-5. The amino acid sequence of PRO213-1 shown in GSeqEdit report starts on page 4 and continues onto the following pages. On page 5, the top sequence is the PRO213 polypeptide sequence and the bottom sequence is the PRO213-1 polypeptide sequence.

15. The amino acid sequence starting on page 6 of the GSeqEdit is identical for both the PRO213 and PRO213-1 polypeptides. Amino acid residue number 35, shown on page 6 of the GSeqEdit report, indicates the continuous numbering of PRO213-1 polypeptide sequence from the previous page. The first amino acid on page 6 corresponds to amino acid 57 of the PRO213 polypeptide.

16. The amino acid sequence of residues 35-273 of SEQ ID NO:506 shown in Figure 213 of the above-identified application is 239 amino acids long, and is identical to the amino acid sequence of residues 57-295 of SEQ ID NO:2 shown in Figure 2 of the above-identified application.

17. The nucleic acid sequence encoding residues 35-273 of SEQ ID NO: 506 comprises residues 501-1220 of SEQ ID NO:505 in Figure 212 of the above-identified application. The nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505 is 720 nucleotides long and it includes a stop codon.

18. The portion of the PRO213 polypeptide, which is identical to the portion of the PRO213-1 polypeptide encoded by the nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505, is significantly homologous with the human growth arrest-specific 6 (gas6) protein.

19. Both DNA30943-1163 cDNA sequence and the PRO213 polypeptide encoded by DNA30943-1163 were obtained prior to June 18, 1997. Furthermore, the homology of PRO213 to human gas6 was obtained prior to June 18, 1997.

20. The DNA sequence of nucleotides 606 to 1223 of SEQ ID NO:1 is identical to nucleotides 603 to 1220 of DNA30943-1-1163-1 sequence shown in the GSeqEdit report. Further, the DNA sequences of nucleotides 606 to 1223 of SEQ ID NO:1 and nucleotides 603 to 1220 of DNA30943-1-1163-1 shown in the GSeqEdit report are identical to that of nucleotides 603-1220 of SEQ ID NO:505 disclosed in the above-identified application.

21. The beginning of the cDNA sequence corresponding to nucleotides 501-1220 of SEQ ID NO:505 in the above-identified application is shown on page 6 of the GSeqEdit database report. The location of nucleotide 501 of SEQ ID:505, which corresponds to nucleotide 501 of DNA30943-1-1163-1 shown in the GSeqEdit report, is marked with an arrow. The location of nucleotide 603 of SEQ ID:505, which corresponds to nucleotide 603 of DNA30943-1-1163-1 shown on page 7 of the GSeqEdit report, is marked with an arrow. The location of the nucleotide 1220 of SEQ ID NO:505, which corresponds to nucleotide 1220 of DNA30943-1-1163-1 shown on page 12 of the GSeqEdit report, is marked with an arrow.

22. The amino acid residues in the GSeqEdit report which correspond to residues 35 to 273 of SEQ ID NO: 506 are shown starting on page 6 (indicated by an arrow) to page 12 of the report.

23. Exhibit A clearly shows that amino acids residues 35 to 273 of SEQ ID NO: 506 and the nucleic acid residues 603-1220 of SEQ ID NO: 505 disclosed in the above-identified application, as well as the homology of the polypeptide to human gas6, were obtained prior to June 18, 1997.

24. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard, Ph.D.	5/8/05 Date
Paul J. Godowski, Ph.D.	Date
Austin Gurney, Ph.D.	Date
Margaret A. Roy	Date
William I. Wood, Ph.D.	Date

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3. The polypeptide comprising the amino acid sequence of residues 35-273 of SEQ ID NO:506 and the nucleic acid sequence of nucleotides 603-1220 of SEQ ID NO:505 in the above-identified application in the United States were sequenced and cloned prior to June 18, 1997.

4. At the time the above polypeptide was cloned and sequenced, one of the inventors, Austin Gurney, was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA encoding the polypeptide comprising the amino acid sequence of residues 35-273 of SEQ ID NO:506.

5. At the time the above polypeptide was cloned and sequenced, one of the inventors, Audrey Goddard, was responsible for overseeing the sequencing of nucleotides encoding novel polypeptides, including the polypeptide having the amino acid sequence of residues 35-273 of SEQ ID NO: 506 in the above-identified application.

6. At the time the nucleotide encoding the above polypeptide was cloned and sequenced, one of the inventors, William I. Wood, was responsible for overseeing the homology searches for novel polypeptides, including that for the polypeptide having the amino acid sequence of residues 35-273 of SEQ ID NO: 506 in the above-identified application.

7. The PRO213 polypeptide shown in SEQ ID NO:2 is encoded by a cDNA sequence referred to as DNA30943-1163 and shown in Figure 2 of the above-identified application.

8. A cDNA sequence DNA30943-1163 is identified as SEQ ID NO:1 and shown in Figure 1 of the above-identified application.

9. The PRO213 nucleic acid sequence was found to contain sequence errors. Therefore, the PRO213 nucleic acid sequence was resequenced and designated as 213-1 nucleic acid sequence and the translated polypeptide was designated as the PRO213-1 polypeptide.

10. The PRO213-1 polypeptide shown in SEQ ID NO:506 is encoded by a cDNA sequence referred to as DNA30943-1-1163-1 and shown in Figure 213 of the above-identified application..

11. A cDNA sequence DNA30943-1-1163-1 is identified as SEQ ID NO:505 and shown in Figure 212 of the above-identified application.

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14. The amino acid sequence of residues 1-49 of PRO213 is shown in GSeqEdit report on pages 4-5. The amino acid sequence of PRO213-1 shown in GSeqEdit report starts on page 4 and continues onto the following pages. On page 5, the top sequence is the PRO213 polypeptide sequence and the bottom sequence is the PRO213-1 polypeptide sequence.

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16. The amino acid sequence of residues 35-273 of SEQ ID NO:506 shown in Figure 213 of the above-identified application is 239 amino acids long, and is identical to the amino acid sequence of residues 57-295 of SEQ ID NO:2 shown in Figure 2 of the above-identified application.

17. The nucleic acid sequence encoding residues 35-273 of SEQ ID NO: 506 comprises residues 501-1220 of SEQ ID NO:505 in Figure 212 of the above-identified application. The nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505 is 720 nucleotides long and it includes a stop codon.

18. The portion of the PRO213 polypeptide, which is identical to the portion of the PRO213-1 polypeptide encoded by the nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505, is significantly homologous with the human growth arrest-specific 6 (gas6) protein.

19. Both DNA30943-1163 cDNA sequence and the PRO213 polypeptide encoded by DNA30943-1163 were obtained prior to June 18, 1997. Furthermore, the homology of PRO213 to human gas6 was obtained prior to June 18, 1997.

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22. The amino acid residues in the GSeqEdit report which correspond to residues 35 to 273 of SEQ ID NO: 506 are shown starting on page 6 (indicated by an arrow) to page 12 of the report.

23. Exhibit A clearly shows that amino acids residues 35 to 273 of SEQ ID NO: 506 and the nucleic acid residues 603-1220 of SEQ ID NO: 505 disclosed in the above-identified application, as well as the homology of the polypeptide to human gas6, were obtained prior to June 18, 1997.

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7. The PRO213 polypeptide shown in SEQ ID NO:2 is encoded by a cDNA sequence referred to as DNA30943-1163 and shown in Figure 2 of the above-identified application.

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9. The PRO213 nucleic acid sequence was found to contain sequence errors. Therefore, the PRO213 nucleic acid sequence was resequenced and designated as 213-1 nucleic acid sequence and the translated polypeptide was designated as the PRO213-1 polypeptide.

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12. Copies of the pages from the GSeqEdit database and GenenGenes database which report the cloning, sequencing and functional data for the PRO213 and PRO213-1 polypeptide sequences, including its homology to human gas6, as well as the cloning, and sequencing data for the nucleic acid sequence encoding the PRO213 and PRO213-1 polypeptides are attached to this declaration (with the dates redacted) as Exhibit A.

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16. The amino acid sequence of residues 35-273 of SEQ ID NO:506 shown in Figure 213 of the above-identified application is 239 amino acids long, and is identical to the amino acid sequence of residues 57-295 of SEQ ID NO:2 shown in Figure 2 of the above-identified application.

17. The nucleic acid sequence encoding residues 35-273 of SEQ ID NO: 506 comprises residues 501-1220 of SEQ ID NO:505 in Figure 212 of the above-identified application. The nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505 is 720 nucleotides long and it includes a stop codon.

18. The portion of the PRO213 polypeptide, which is identical to the portion of the PRO213-1 polypeptide encoded by the nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505, is significantly homologous with the human growth arrest-specific 6 (gas6) protein.

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20. The DNA sequence of nucleotides 606 to 1223 of SEQ ID NO:1 is identical to nucleotides 603 to 1220 of DNA30943-1-1163-1 sequence shown in the GSeqEdit report. Further, the DNA sequences of nucleotides 606 to 1223 of SEQ ID NO:1 and nucleotides 603 to 1220 of DNA30943-1-1163-1 shown in the GSeqEdit report are identical to that of nucleotides 603-1220 of SEQ ID NO:505 disclosed in the above-identified application.

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22. The amino acid residues in the GSeqEdit report which correspond to residues 35 to 273 of SEQ ID NO: 506 are shown starting on page 6 (indicated by an arrow) to page 12 of the report.

23. Exhibit A clearly shows that amino acids residues 35 to 273 of SEQ ID NO: 506 and the nucleic acid residues 603-1220 of SEQ ID NO: 505 disclosed in the above-identified application, as well as the homology of the polypeptide to human gas6, were obtained prior to June 18, 1997.

24. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard, Ph.D.	Date
Paul J. Godowski, Ph.D.	Date
Austin Gurney, Ph.D.	Date
Margaret A. Roy	3 May 2005 Date
William I. Wood, Ph.D.	Date

SV 2094833 v1
5/1/05 2:23 PM (39780.2630)

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants:	Goddard et al.	Attorney's Docket No: 39780-2630P1C4
Serial No:	09/978,191	Group Art Unit: 1646
Filed:	October 15, 2001	Examiner: O'Hara, Eileen B.

For: **SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME**

Commissioner for Patents
P.O. Box 1450
Alexandria, Virginia 22313-1450

DECLARATION OF AUDREY GODDARD, Ph.D., PAUL J. GODOWSKI, Ph.D., AUSTIN GURNEY, Ph.D., MARGARET A. ROY and WILLIAM I. WOOD, Ph.D.UNDER 37 CFR 1.131

We, Audrey Goddard, Ph.D., Paul J. Godowski, Ph.D., Austin Gurney, Ph.D., Margaret Roy and William I. Wood, Ph.D. do hereby declare and say as follows:

1. We are the inventors of the above-identified application.

2. We have read and understood the claims pending in this application, and are aware that the claims have been rejected as anticipated by Holtzman *et al.*, U.S. Published Patent Application 20020028508, with effective priority date April 23, 1998 (09/065,363), and Sheppard *et al.*, U.S. Published Patent Application 20030166907, with effective priority date June 18, 1997 (09/050,143)

3. The polypeptide comprising the amino acid sequence of residues 35-273 of SEQ ID NO:506 and the nucleic acid sequence of nucleotides 603-1220 of SEQ ID NO:505 in the above-identified application in the United States were sequenced and cloned prior to June 18, 1997.

4. At the time the above polypeptide was cloned and sequenced, one of the inventors, Austin Gurney, was responsible for overseeing the cloning of cDNAs which encoded novel polypeptides, including the cDNA encoding the polypeptide comprising the amino acid sequence of residues 35-273 of SEQ ID NO:506.

5. At the time the above polypeptide was cloned and sequenced, one of the inventors, Audrey Goddard, was responsible for overseeing the sequencing of nucleotides encoding novel polypeptides, including the polypeptide having the amino acid sequence of residues 35-273 of SEQ ID NO: 506 in the above-identified application.

6. At the time the nucleotide encoding the above polypeptide was cloned and sequenced, one of the inventors, William I. Wood, was responsible for overseeing the homology searches for novel polypeptides, including that for the polypeptide having the amino acid sequence of residues 35-273 of SEQ ID NO: 506 in the above-identified application.

7. The PRO213 polypeptide shown in SEQ ID NO:2 is encoded by a cDNA sequence referred to as DNA30943-1163 and shown in Figure 2 of the above-identified application.

8. A cDNA sequence DNA30943-1163 is identified as SEQ ID NO:1 and shown in Figure 1 of the above-identified application.

9. The PRO213 nucleic acid sequence was found to contain sequence errors. Therefore, the PRO213 nucleic acid sequence was resequenced and designated as 213-1 nucleic acid sequence and the translated polypeptide was designated as the PRO213-1 polypeptide.

10. The PRO213-1 polypeptide shown in SEQ ID NO:506 is encoded by a cDNA sequence referred to as DNA30943-1-1163-1 and shown in Figure 213 of the above-identified application..

11. A cDNA sequence DNA30943-1-1163-1 is identified as SEQ ID NO:505 and shown in Figure 212 of the above-identified application.

12. Copies of the pages from the GSeqEdit database and GenenGenes database which report the cloning, sequencing and functional data for the PRO213 and PRO213-1 polypeptide sequences, including its homology to human gas6, as well as the cloning, and sequencing data for the nucleic acid sequence encoding the PRO213 and PRO213-1 polypeptides are attached to this declaration (with the dates redacted) as Exhibit A.

13. The GSeqEdit report shows the full-length nucleic acid sequence for DNA30943-1-1163-1 and the full-length PRO213-1 polypeptide encoded by DNA30943-1-1163-1. The full-length nucleic acid sequence for PRO213-1 (DNA30943-1-1163-1) shown in the report includes the sequence corrections made to PRO213 (DNA30943-1163) indicated below the sequence, for example, as seen on page 5 of the report. The full-length nucleic acid sequence for PRO213 (DNA30943-1163) is the sequence shown in the GSeqEdit report without the indicated corrections.

14. The amino acid sequence of residues 1-49 of PRO213 is shown in GSeqEdit report on pages 4-5. The amino acid sequence of PRO213-1 shown in GSeqEdit report starts on page 4 and continues onto the following pages. On page 5, the top sequence is the PRO213 polypeptide sequence and the bottom sequence is the PRO213-1 polypeptide sequence.

15. The amino acid sequence starting on page 6 of the GSeqEdit is identical for both the PRO213 and PRO213-1 polypeptides. Amino acid residue number 35, shown on page 6 of the GSeqEdit report, indicates the continuous numbering of PRO213-1 polypeptide sequence from the previous page. The first amino acid on page 6 corresponds to amino acid 57 of the PRO213 polypeptide.

16. The amino acid sequence of residues 35-273 of SEQ ID NO:506 shown in Figure 213 of the above-identified application is 239 amino acids long, and is identical to the amino acid sequence of residues 57-295 of SEQ ID NO:2 shown in Figure 2 of the above-identified application.

17. The nucleic acid sequence encoding residues 35-273 of SEQ ID NO: 506 comprises residues 501-1220 of SEQ ID NO:505 in Figure 212 of the above-identified application. The nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505 is 720 nucleotides long and it includes a stop codon.

18. The portion of the PRO213 polypeptide, which is identical to the portion of the PRO213-1 polypeptide encoded by the nucleic acid sequence comprising residues 501-1220 of SEQ ID NO:505, is significantly homologous with the human growth arrest-specific 6 (gas6) protein.

19. Both DNA30943-1163 cDNA sequence and the PRO213 polypeptide encoded by DNA30943-1163 were obtained prior to June 18, 1997. Furthermore, the homology of PRO213 to human gas6 was obtained prior to June 18, 1997.

20. The DNA sequence of nucleotides 606 to 1223 of SEQ ID NO:1 is identical to nucleotides 603 to 1220 of DNA30943-1-1163-1 sequence shown in the GSeqEdit report. Further, the DNA sequences of nucleotides 606 to 1223 of SEQ ID NO:1 and nucleotides 603 to 1220 of DNA30943-1-1163-1 shown in the GSeqEdit report are identical to that of nucleotides 603-1220 of SEQ ID NO:505 disclosed in the above-identified application.

21. The beginning of the cDNA sequence corresponding to nucleotides 501-1220 of SEQ ID NO:505 in the above-identified application is shown on page 6 of the GSeqEdit database report. The location of nucleotide 501 of SEQ ID:505, which corresponds to nucleotide 501 of DNA30943-1-1163-1 shown in the GSeqEdit report, is marked with an arrow. The location of nucleotide 603 of SEQ ID:505, which corresponds to nucleotide 603 of DNA30943-1-1163-1 shown on page 7 of the GSeqEdit report, is marked with an arrow. The location of the nucleotide 1220 of SEQ ID NO:505, which corresponds to nucleotide 1220 of DNA30943-1-1163-1 shown on page 12 of the GSeqEdit report, is marked with an arrow.

22. The amino acid residues in the GSeqEdit report which correspond to residues 35 to 273 of SEQ ID NO: 506 are shown starting on page 6 (indicated by an arrow) to page 12 of the report.

23. Exhibit A clearly shows that amino acids residues 35 to 273 of SEQ ID NO: 506 and the nucleic acid residues 603-1220 of SEQ ID NO: 505 disclosed in the above-identified application, as well as the homology of the polypeptide to human gas6, were obtained prior to June 18, 1997.

24. We hereby declare that all statements made herein of our own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

Audrey Goddard, Ph.D.	Date
Paul J. Godowski, Ph.D.	Date
Austin Gurney, Ph.D.	Date
Margaret A. Roy	Date
William I. Wood, Ph.D.	4/29/05 Date

SV 2094833 v1
4/29/05 10:13 AM (39780.2630)

>Wednesday, [redacted]
>DNA30943 [Full]
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                                           nciI
                                           mspI
                                           hpaII    mnlI
                                           dsaV  sau3AI rmaI
                                           bssKI mboI/ndeII[dam-]
                                          xmaI/pspAI    maeI
      sau96I[dcm-]                        smaI   dpnII[dam-]
      avaII[dcm-]                         scrFI[M.hpaII-]
    scrFI[dcm-]                           nciI   dpnI[dam+]
    pspGI                                 dsaV  nlaIV xbaI   sau3AI taqI          hgaI
    mvaI                              tsp509I[M.ecoRI-]  bfaI mboI/ndeII[dam-]    thaI    mwoI
    ecoRII[dcm-]                     ecoRI bssKI bstYI/xhoII  dpnII[dam-]         fnuDII/mvnI      sau96I[M.ha
    dsaV[dcm-]                       apoI  bsaJI bamHI hpy188III  mnlI            bstUI   bglI[M.haeIII-]  bce
    bstNI          mnlI          taqI[M.claI-] bsaJI alwI[dam-]  dpnI[dam+]    drdI  bsh1236I     mwoI     hpyCH4
    bssKI[dcm-] hpyCH4V         claI/bsp106    avaI[M.hpaII-]    alwI[dam-]  taqI   mluI eciI    cac8I   bsgI
    apyI[dcm+] bsgI bsaJI       bspDI[dam-]  bsaJI  alwI[dam-]  bstYI/xhoII mnlI    aflIII aciI  aluI haeIII/palI
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    GGTCCAGGTT GACGTGGAGC CAAGATAGCT AACTTAAGGG GCCCCTAGGA GATCTCTAGG GAGCTGGAGC TGGGTGCGCA GGCGGTTCGA CCGGGACGTG
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                                    pspGI                             ecoRII[dcm-]               haeIII/palI
                                    mvaI bspMI      ddeI              dsaV[dcm-]                eco0109I/draII
                                    ecoRII[dcm-]    bspCNI nlaIV      bstNI eaeI               mnlI
                                    dsaV[dcm-]     mnlI  mnlI         bssKI[dcm-]             ddeI                  sau96I
       mwoI                         bstXI[M.haeIII-] hpy188III        apyI[dcm+]              bspCNI  bslI          avaII
        hpyCH4V                     bstNI          eco81I  banI mnlI    cfrI                 eco81I bslI           nlaIV
      tseI       nlaIV              bssKI[dcm-]    bsu36I/mstII/sauI  fnu4HI/bsoFI bsu36I/mstII/sauI             rmaI
      fnu4HI/bsoFI                  apyI[dcm+]  haeIII/palI    bslI   aciI tspRI haeIII/palI                     maeI
      bbvI      mnlI               haeIII/palI  sau96I[M.haeIII-] bpmI/gsuI[dcm-] sau96I[M.haeIII-]              bfaI
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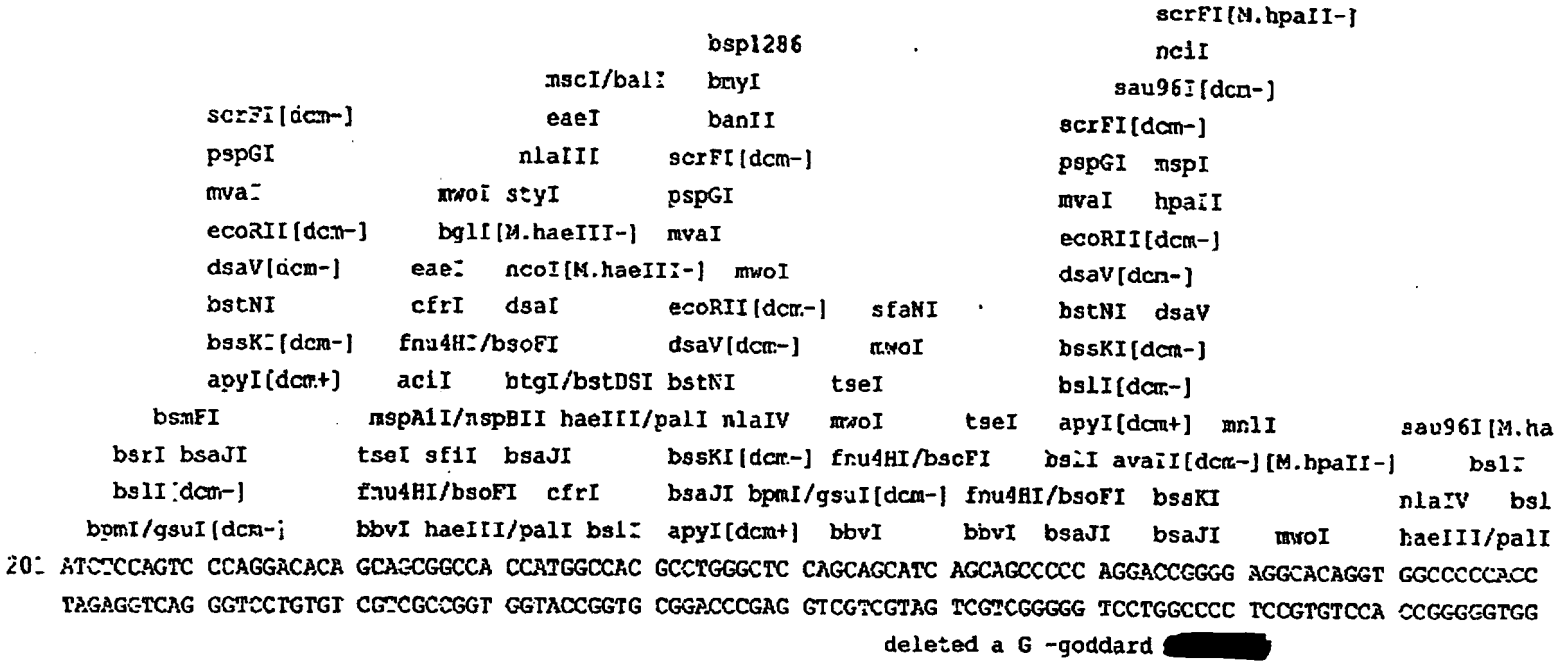
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bpmI/gsuI[dcm-]
bbvI haeIII/palI
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apyI[dcm+]
bbvI
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bsaJI
mwoI
haeIII/palI
201 ATCTCCAGTC CCAGGACACA GCAGCGGCCA CCATGGCCAC GCCTGGGCTC CAGCAGCATC AGCAGCCCCC AGGACCGGGG AGGCACAGGT GGCCCCCACC
TAGAGGTCAG GGTCCTGTGT CGTCGCCGGT GGTACCGGTG CGGACCCGAG GTCGTCGTAG TCGTCGGGGG TCCTGGCCCC TCCGTGTCCA CCGGGGGTGG
deleted a G -goddard

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    mspI  tseI           nciI           aciI   haeIII/palI                    bstNI
    hpaII mwoI           mspI          eciI dsaV[dcm-]                        bssKI[dcm-]
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   dsaV  bstAPI    bslI bssKI fokI bsaXI bseRI apyI[dcm+]  mnlI            aciI   mnlI   haeIII/
   bssKI bbvI      bslI bsaJI bstF5I hinfI bslI[dcm-] bslI bseRI   haeIII/palI bpmI/gsuI[dcm-]
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    TGGGCCTCCT CGTCGAGGAC GGGGACAGGC CCCCTACTGA CTAAGAGGAG GCGGTCCGGT GGGTCTCCTC TTCCGGTGGG GCGGACCTCC GTGTCCGGTA
 1                               M  T  D  S  P  P  P  G  H  P  E  E  K  A  T  P  P  G  G  T  G  H
 1                                                                                                 N
                                                                                        Correct ORF^
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                                                                                                    bceAI
                                                                                                   haeIII/palI
                                                                                                  mcrI
                                                                                                  eagI/xmaIII/eclXI
                                                                                                  eaeI
                                                                                                  cfrI
                                                                                                  bsiEI
                                                                                                 mspI[M.haeIII-]
                                                                                                 hpaII
                                                                                                scrFI[M.hpaII-]        bsp
                                                                                                nciI                   bmy
                                                                                                dsaV                   ban
                                                                                  cac8I         bssKI                 scrFI
                                                                                hgiAI/aspHI   sau96I[M.haeIII-]       nciI
      bsp1286            mwoI                                                   bsp1286       haeIII/palI             mspI
      bmyI ddeI  mnlI tseI                                                      bsiHKAI     mspI[M.haeIII-]           hpaII
      banII hpy188III fnu4HI/bsoFI                                   tspRI  fnu4HI/bsoFI     hpaII bslI               dsaV
   mnlI    bspCNI     bbvI                                          btsI   aciI    bmyI    cfr10I/bsrFI            mwoI bssKI
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 23 E  G  L  S   G  G  A   A  D  V   A  S  G  V   G  S  G   R  H  R   A  R  L  P   A  R  P  O
  2  R  G  S   Q  E  V  L   L  M  W   L  L  V   L  A  V  G   G  T  E   H  A  Y   R  P  G  R   R  V  C   A  V  R
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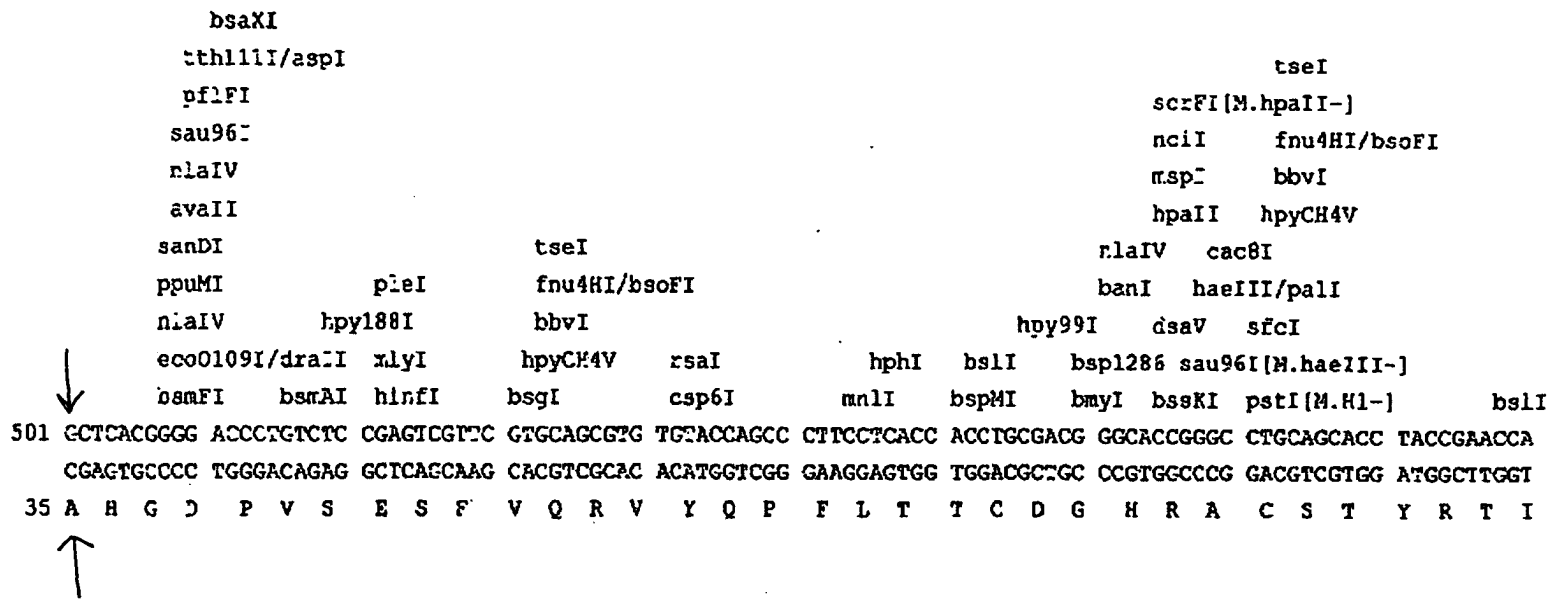
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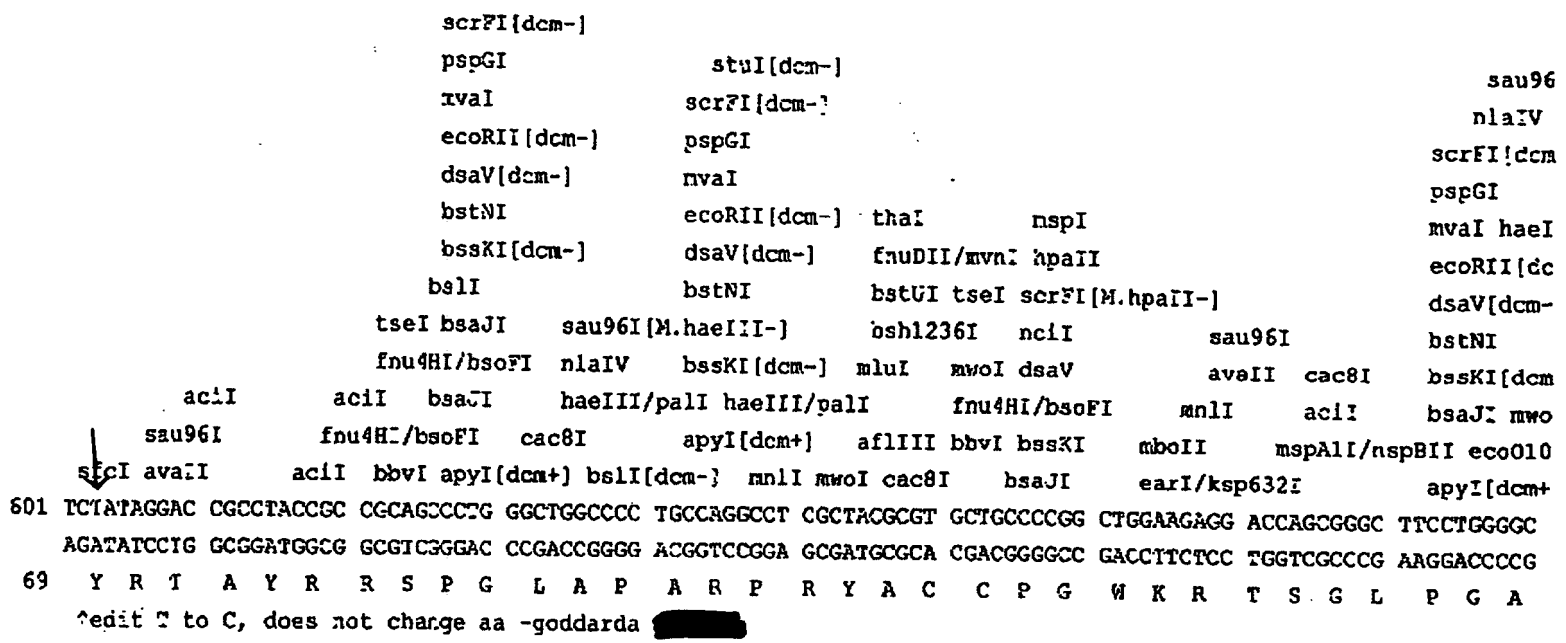
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edit T to C, does not change aa -goddarda [redacted]

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                                                                                   mwoI
                                                                               mwoI
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                                                                             cfrI  fnu4HI/bsoFI
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                                                                            pspGI   bbvI  tseI   sfcI
                                                                            mvaI  mspA1I/nspBII  pstI
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102 C  G  A   A  I  C  Q   P  P  C   R  N  G   G  S  C  V   Q  P  G   R  C  R   C  P  A  G   W  R  G   D  T  C

                                                               tseI                 alwNI[dcm-]
                                                               fnu4HI/bsoFI      mspI
                                                               bbvI              hpaII       nlaIV
                                            rmaI             hinPI sfaNI        naeI/ngoMI bsrI
                              bsmI  tspRI     mnlI           hhaI/cfoI          cfr10I/bsrFI  banI  tspRI        bspi286
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                   hpy188I  bstF5I hpyCH4V bfaI      aciI    bsmFI afeI/eco47III   aciI   alw26I/bsmAI  bslI     mnlI
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135 Q  S  D  V   D  E  C   S  A  R   R  G  G  C   P  Q  R   C  I  N   T  A  G  S   Y  W  C   Q  C  W   E  G  H  S
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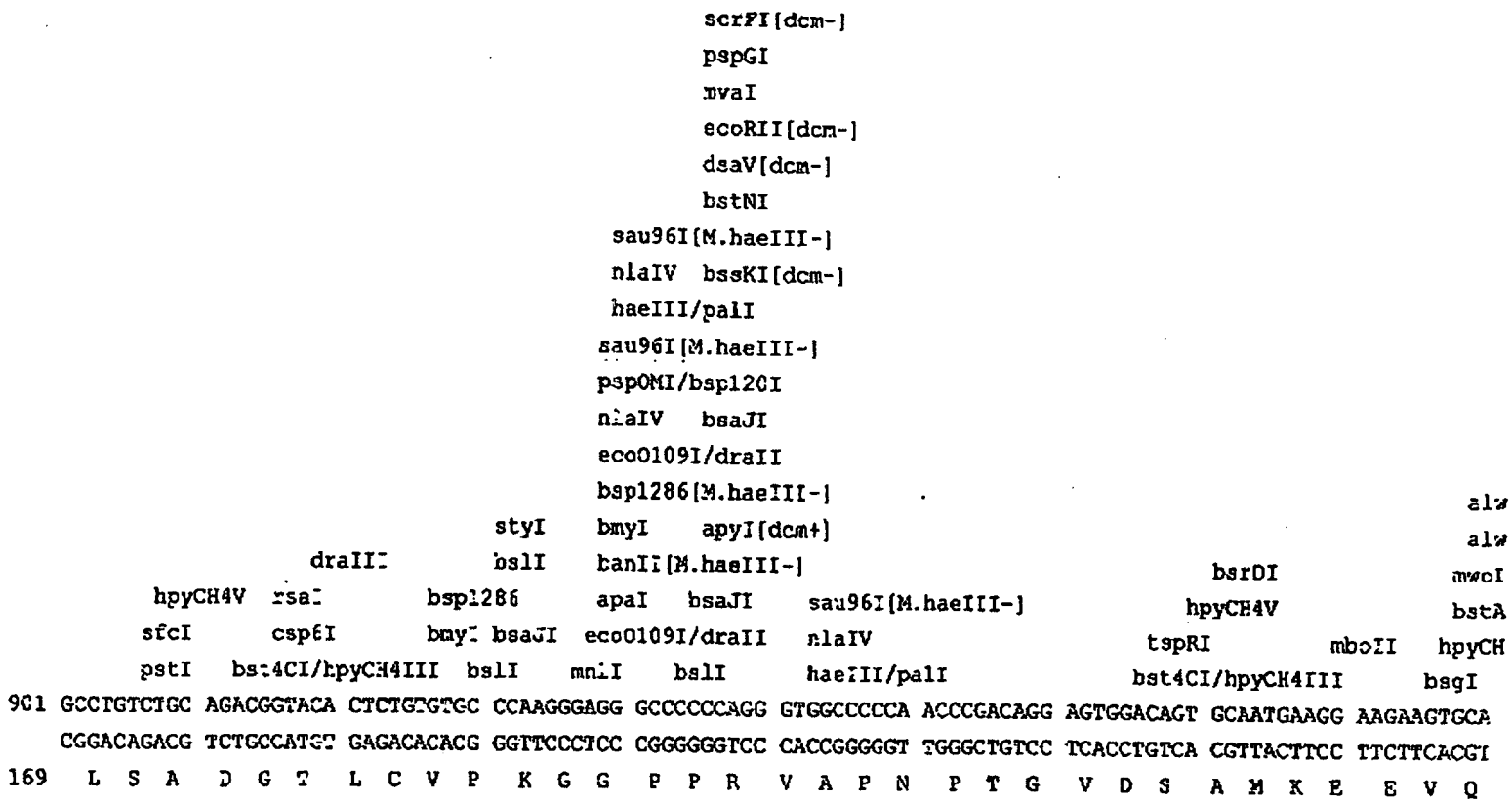
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ecoRII[dcm-]
dsaV[dcm-]
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sau96I[M.haeIII-]
nlaIV bssKI[dcm-]
haeIII/palI
sau96I[M.haeIII-]
pspOMI/bsp120I
nlaIV bsaJI
eco0109I/draII
bsp1286[M.haeIII-]
styI bmyI apyI[dcm+]
draIII bslI banII[M.haeIII-]
hpyCH4V rsaI bsp1286 apaI bsaJI sau96I[M.haeIII-]
sfcI csp6I bmyI bsaJI eco0109I/draII nlaIV
pstI bst4CI/hpyCH4III bslI mnlI bslI haeIII/palI
alw
alw
bsrDI
mwoI
hpyCH4V
bstA
tspRI mboII hpyCH
bst4CI/hpyCH4III bsgI
901 GCCTGTCTGC AGACGGTACA CTCTGCGTGC CCAAGGGAGG GCCCCCCAGG GTGGCCCCCA ACCCGACAGG AGTGGACAGT GCAATGAAGG AAGAAGTGCA
CGGACAGACG TCTGCCATGT GAGACACACG GGTTCCCTCC CGGGGGGTCC CACCGGGGGT TGGGCTGTCC TCACCTGTCA CGTTACTTCC TTCTTCACGT
169 L S A D G T L C V P K G G P P R V A P N P T G V D S A M K E E V Q

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                                        tseI
            scrFI[dcn-]                 mwoI
            pspGI                       fnu4HI/bsoFI
            mvaI                        bstAPI                                  mwoI                                sa
            ecoRII[dcn-]                bbvI                            scrFI[dcm-]                             mspI
            dsaV[dcn-]                  hpyCH4V       sau96I[M.haeIII-] haeIII/palI                             scrFI
            bstNI                       sfcI          nlaIV             pspGI     cac8I                           nciI
      sfcI  bssKI[dcm-]                 pstI[M.aluI-][M.Hl-]            mvaI bglI[M.haeIII-]          nlaIV nl
      pstI[M.Hl-]       ecoNI           tseI  aluI[M.pstI-]     hpyCH4V eccRII[dcm-]      bpmI/gsuI[dcm-] hpaI
     tseI    bsaJI    bspMI             fnu4HI/bsoFI    haeIII/palI     dsaV[dcm-]       bsrI       bsp1286 av
     fnu4HI/bsoFI  sau96I    mnlI        bbvI pvuII[M.Hl-]       bsgI    bstNI mnlI alwNI[dcm-]      bmyI dsaV
     bbvI    apyI[dcm-] bslI  bseRI   aluI[M.pstI-] cac8I    tspRI     bssKI[dcm-]     tspRI       banII bslI
   mnlI hpyCH4V       avaII  bpmI/gsuI[dcm-] mspAlI/nspBII   btsI      apyI[dcm+] alw26I/bsmAI nlaIII   bsaKI
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     CTCCGACGTC AGGTCCCACC TGGACGACCT CCTCTTCGAC GTCGACCACG ACCGGGGTGA CGTGTCGGAC CGGAGCGTCC GTGACCTCGT ACCCGAGGGC
 202  R  L  Q   S  R  V  D   L  L  E   E  K  L   Q  L  V  L   A  P  L   H  S  L   A  S  Q   A   L  E  H   G  L  P
```

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                    bglAI/aspEI
                    bsp1286
                    bsiEHKAI
                    bmyI
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          tseI   pspGI                                                       bseRI
          fnu4HI/bsoFI                    aciI                            bpmI/gsuI[dcm-]
          bbvI   mvaI hpyCH4V             fnu4HI/bsoFI                    scrFI[dcm-]        sau96I
       mspI      ecoRII[dcm-]           ncrI      pleI                     pspGI     tseI     avaII
       hpaII     dsaV[dcm-]             eagI/xmaIII/eclXI                  mvaI      fnu4HI/bsoFI
      scrFI[M.hpaII-] apaLI/snoI        eaeI      mlyI                     ecoRII[dcm-]      ppuMI
      nciI      bstNI                 aluI haeIII/palI        cac8I       dsaV[dcm-] pvuII[M.HI-]
      dsaV      bssKI[dcm-]         tseI  cfrI      hinfI[M.taqI-]        bstNI     bbvI    nlaIV
      bssKI     apyI[dcm-]          fnu4HI/bsoFI  taqI    ddeI            bssKI[dcm-] aluI  eco0109I/dr
     bsaJI    mnlI  alw44I/snoI     bbvI  bsiEI sfaNI     bspCNI          apyI[dcm+] mspA1I/nspBII
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     CTGGGGCCGT CGGAGGACCA CGTGAGGAAG GTCGTCGAGC CGGCGTAGCT GAGGGACTCG CTCGTCTAAA GGAAGGACCT CCTCGTCGAC CCCAGGACGA
 235 D  P  G  S  L  L  V  H  S  F  Q  Q  L  G  R  I  D  S  L  S  E  Q  I  S  F  L  E  E  Q  L  G  S  C  S
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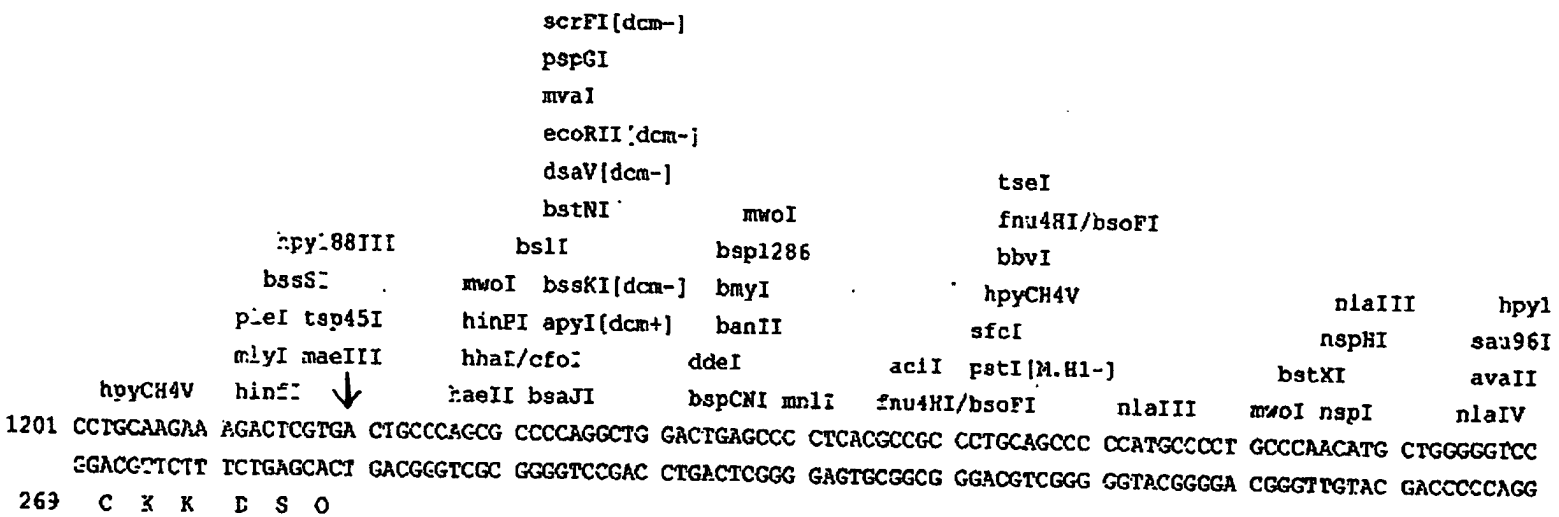
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bmyI
hpyCH4V
nlaIII
hpyI
pleI tsp45I
hinPI
apyI[dcm+]
banII
sfcI
nspHI
sau96I
mlyI maeIII
hhaI/cfoI
ddeI
aciI
pstI[M.H1-]
bstXI
avaII
hpyCH4V
hinfI
haeII bsaJI
bspCNI mnlI
fnu4HI/bsoFI
nlaIII
mwoI nspI
nlaIV
1201 CCTGCAAGAA AGACTCGTGA CTGCCCAGCG CCCCAGGCTG GACTGAGCCC CTCACGCCGC CCTGCAGCCC CCATGCCCCT GCCCAACATG CTGGGGGTCC
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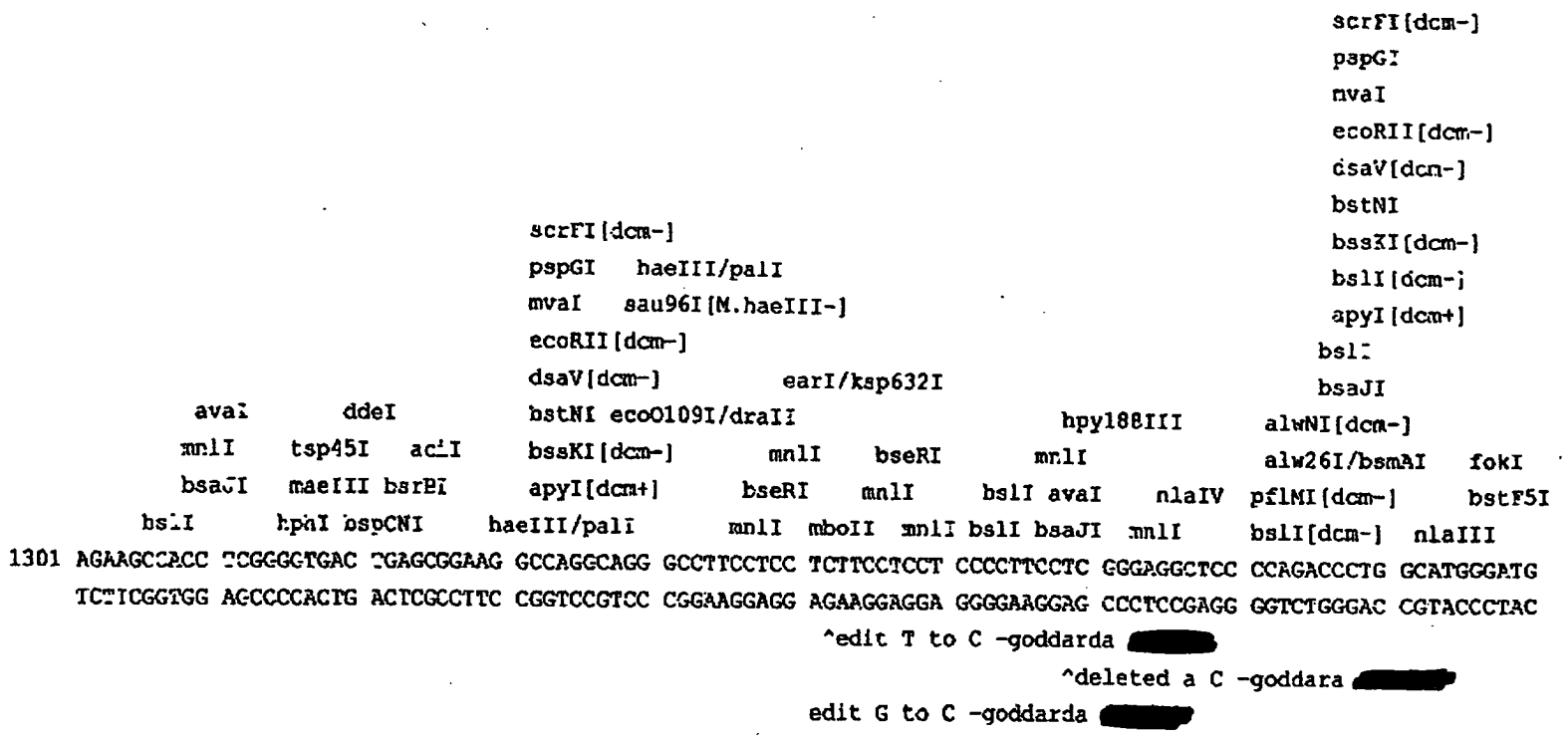
269 C K K D S Q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bssKI[dcm-]
bslI[dcm-]
apyI[dcm+]
bslI
bsaJI
alwNI[dcm-]
alw26I/bsmAI
fokI
pflMI[dcm-]
bstF5I
bslI[dcm-]
nlaIII
scrFI[dcm-]
pspGI haeIII/palI
mvaI sau96I[M.haeIII-]
ecoRII[dcm-]
dsaV[dcm-]
earI/ksp632I
bstNI eco0109I/draII
bssKI[dcm-]
apyI[dcm+]
aval
ddeI
mnlI
tsp45I
aclI
bsaJI
maeIII
bsrBI
bslI
hpaI
bspCNI
haeIII/palI
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bseRI
mnlI
bseRI
mnlI
bslI
avaI
nlaIV
mnlI
mboII
mnlI
bslI
bsaJI
mnlI
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1301 AGAAGCCACC TCGGGGTGAC TGAGCGGAAG GCCAGGCAGG GCCTTCCTCC TCTTCCTCCT CCCCTTCCTC GGGAGGCTCC CCAGACCCTG GCATGGGATG
TCTTCGGTGG AGCCCCACTG ACTCGCCTTC CGGTCCGTCC CGGAAGGAGG AGAAGGAGGA GGGGAAGGAG CCCTCCGAGG GGTCTGGGAC CGTACCCTAC
^edit T to C -goddarda
^deleted a C -goddara
edit G to C -goddarda

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                                                                                                            sau96I[M.haeIII-]
                                                                                                            haeIII/palI
                                                                                                           sau96I[M.haeIII-]
                                                   nlaIV                                                   pspOMI/bsp120I
                                                   kpnI                                                    nlaIV
                                                   banI                                             scrFI[dcm-]
                                                   asp718                                           pspGI   eco0109I/draII
                                                scrFI[dcm-]                                         mvaI    bsp1286[M.haeIII-]        ss
                                                pspGI                                               ecoRII[dcm-]                      sa
                                    scrFI[dcm-]  mvaI rsaI                                          dsaV[dcm-]                        hg
                                    pspGI        ecoRII[dcm-]                                       bstNI   bmyI      ddeI[M.aluI-]   ec
          mboII                     mvaI         dsaV[dcm-]                                         bssKI[dcm-]       bspCNI          bs
         sau3AI                     ecoRII[dcm-] bstNI                                             mwoI    banII[M.haeIII-]           bs
         xboI/ndeII[dam-]           dsaV[dcm-]   bssKI[dcm-]                                      sfiI[dcm-]      pvuII               bm
         dpnII[dam-]                bstNI        bsaJI                                   fokI styI bglI[M.haeIII-] mspAlI/napBII      ba
         dpnI[dam+]                 bssKI[dcm-]  apyI[dcm+]                              bstF5I  haeIII/palI  ddeI[M.aluI-]          bcg
        bstYI/xhoII    tfiI         apyI[dcm+] bslI bsaJI csp6I                         sfaNI bslI[dcm-]  apaI  bspCNI mnlI       rsaI
        alwI[dam-]     hinfI       bsaJI      bslI[dcm-] acc65I    bceAI   bsaJI apyI[dcm+] mnlI aluI                             csp6I
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          ^edit T to C -goddarda [redacted]
             ^edit T to C -goddarda [redacted]
               ^edit T to C -goddarda [redacted]
```

```
                        sau96I
                        nlaIV
                        avaII
                       sanDI
                       ppuMI
                       nlaIV                    mspI
                       eco0109I/draII        tseI  hpaII
                    scrFI[dcm-]              fnu4HI/bsoFI
                    pspGI     nlaIII         bbvI scrFI[M.hpaII-]
                    mvaI      styI        scrFI[dcm-]
                    ecoRII[dcm-]          pspGI    nciI                tspRI
                    dsaV[dcm-]            mvaI     dsaV               ddeI
                    bstNI     ncoI        ecoRII[dcm-]               mnlI          tseI
                    bssKI[dcm-]           dsaV[dcm-]                 bslI          fnu4HI/bsoFI
                    bsaJI     dsaI        bstNI    bssKI           haeIII/palI    tseI
                    apyI[dcm+]            bssKI[dcm-]  mnlI        sau96I[M.haeIII-]  bbvI
                 nlaIV  bsmFI btgI/bstDSI  apyI[dcm+]  bsaXI      nlaIV bspCNI     fnu4HI/bsoFI
     aluI     bpmI/gsuI[dcm-] bsaJI      haeIII/palI bslI          eco0109I/draII   bbvI
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       ^edit T to C -goddarda[redacted]
            ^deleted a C -goddarda[redacted]
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                                                                                        rmaI
                                                                                        maeI
                                                                                    pleI
                                                                               aciI mlyI                                              sa
                                                                              fnu4HI/bsoFI                                        styI
                                                                             haeIII/palI                                       aciI   ha
                                                                            mcrI    hinfI      taqI                          mwoI nlaII
                                                                            eagI/xmaIII/eclXI salI   hpyCH4V                 fnu4HI/bso
                                                                            eaeI thaI  xbaI pleI    sfcI                     sfiI ncoI[M
                                                                            cfrI fnuDII/mvnI  hincII/hindII[M.taqI-]         dsaI
                                                                            bsiEI   drdI    mlyI    pstI           eaeI      btgI/b
                                                                           notI  bstUI hpy188III  bspMI            cfrI      bsaJI
        taiI                                                               fnu4HI/bsoFI bfaI  accI[M.taqI-] aluI   haeIII/palI
        maeII/hpyCH4IV                                                     aciI  bsh1236I   hinfI[M.taqI-] hindIII bglI[M.hae
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                  aluI
                 taeI
                 fnu4HI/bsoFI
                 bbvI  psiI
                hpyCH4V       maeIII
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     CGGGTTGAAC AAATAACGTC GAATATTACC AATGTTTA
```

> Length: 1738

acc65I(GGTACC):

DNA30943

DNA Info Project DNA28735

Is Primarydna C

Source Info 187 FLS 339 LIB25 RNA22 SRC18 Human Fetal Lung

Gene Info PRO213 Human Egfl7 (VEMF) Non-Secreted UNQ187

Gene Annotation

Genome Mapping Run Geode

Affy
HGU133A 218825_at
HGU133P 218825_at
HGU95C 48695_at
Hu35KA R39467_f_at
Hu35KC RC_N74686_f_at
Hu35KD RC_N70081_at
HuGenen1 NM_016215_at
MOE430A 1421335_a_at, 1435823_x_at, 1451427_a_at, 1451428_x_at
MOE430P 1421335_a_at, 1435823_x_at, 1451427_a_at, 1451428_x_at
Rat230v2 1370402_at, 1374570_at, 1393427_s_at

Agilent
H1Av2 A_23_P123785
H1A A_23_P123785
H1Av2 A_23_P123785
H1B A_32_P210642, A_32_P300230
M1A A_51_P315841
WHG A_32_P210642

FANTOM Mouse:0610012G11

GenBank Human:AB125649, AF186111, AL512735, AY358901, AY358902, AY358903, BC012377
Mouse:AF184973, AK002601, AY239289, AY239290, AY309459, BC024610

GeneHub Human:GENE7437
Mouse:MGENE1470

INCYFL Human:931424.FL1_0, 931424.FL3_0

Incyte Human:416842.1, 416842.13, 416842.17, 416842.56, 416842.58, 416842.62, 416842.64, 416842.67, 416842.68, 416842.69, 416842.70, 416842.72, 416842.74, 984053.1

LocusLink Human:51162
Mouse:353158

MGI Mouse:2449823

OMIM Human:608582

Proteome Human:NP_958854.1
Mouse:NP_942017.1

RefSeq Human:NM_016215, NM_201446
Mouse:NM_178444, NM_198724, NM_198725

UniGene Human:Hs.91481
Mouse:Mm.268933

General Info

Lab Name 28735.2
Insert Name undeterminated
Generated By Full Length Screen
Type of DNA FLS
Insert ID Novel
Action Drp Not FL
Concentration
Origene Plate

Construct Info

Tag
Bases to Sequence

Insert (Digest) Size(bp) 1600
Reverse Size(bp) 1
Internal Size(bp) 239
Cut Size(bp)
Vector
Interest not reviewed
Origene CloneId
Origene Well

Exp System
Sequence Status

DNA30943

Antibody Info No antibody info

Other Info ☐ In Situ image available ☐ TaqMan Hit ☐ Transgenic Animal Model

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	OLI5280	
	OLI5290	
	OLI5572	30943.f1
	OLI5573	30943.f2
	OLI7839	30943.tm.f1
	OLI7840	30943.tm.r1
	OLI7841	30943.tm.p1
	OLI7845	30943.tm.f3
	OLI7846	30943.tm.r3
	OLI7847	30943.tm.p3

Comments

Login	Date Entered	Annotation
dfb	[redacted]	homolog to an unknown human protein and to gas6. The mouse protein with 40 % identity clearly has a signal sequence wheras this clone does not. I think the clone is suspect.-ALG
goddarda	[redacted]	Sequencing in clone 64908 allowed us to correct three sequencing errors in 30943 which lie in the 5' UTR of the gene. However the presence of these errors caused us to identify the wrong 5' end of the ORF in the gene. -goddarda
goddarda	[redacted]	Sequence was flagged as poor quality during proofreading. Tried to rerun reactions with Big DYE chemistry, but too little DNA - signal unreadable. Requested more DNA[redacted] Never received -goddarda
goddarda	[redacted]	amplifiedcolon tumors and to a lesser extent in lung tumors- TaqMan assay
jean	[redacted]	Clone 30943 from plasmid inventory plate is verified correct through partial sequencing

Legal Status No legal status

Status

Scientist Daryl Baldwin

Notebook 0

Page

Storage Location

Box

Slot

Inventory Status

Others ☐ Sent to pLASMID Archive ☐ Clone Verified

Date Entered [redacted]

Date Updated [redacted]

Date Completed

Date Canceled

Cancel Reason

Clone Status not reviewed

Sequence Status

Project Member

No Project member generated

FLS FLSDNA

No FLS, FLSDNA generated

Exp Construct

EXP	Lab Name	Construct DNA	System
EXP7559	Protein Engineering	DNA346527	Baculovirus

ABI

ABI Run.Lane	Date Sequenced	ABI Plate
ABI512.31	[redacted]	
ABI512.32		
ABI512.33		
ABI512.34		
ABI512.35		
ABI812.30		
ABI812.31		
ABI1055.40		
ABI1055.41		
ABI2530.13		1252

MA Plate

MA Plate	Well Num	Well Location	Date	Tyep Plate
PLT129	25	C1	08/11/1999	Inventory

Print Run

No Print run generated

XPT

[redacted]